AMENDMENTS TO THE CLAIMS

The following listing of claims replaces all prior versions and listings of claims in this application:

Claims 1-108. (Cancelled)

109. (Currently Amended) A method for monitoring synthesis of one or more proteins which comprises:

binding a first label to at least one ribosome or a fragment thereof to form a donor fluorophore;

binding a second label to at least one tRNA to form an acceptor fluorophore;

detecting electromagnetic radiation signals emitted when the first and second labels are in proximity, wherein the signals are obtained from the donor and acceptor fluorophores forming a fluorescence resonance energy transfer (FRET) pair, with the signals indicating progression of the synthesis of the one or more proteins; and

analyzing the detected signals to identify one or more proteins being synthesized by producing a FRET signal from the FRET pair, computing a synthesis signal from the FRET signal, and interrogating a database compiled from signal data of various FRET pairs so as to identify the one or more proteins that most likely have produced the detected signals.

110. (Previously Presented) The method of claim 109, wherein the emitted radiation signals comprises radiation obtained by energy transfer between the first label which is covalently bound to the at least one ribosome or fragment thereof and the second label which is covalently bound to the at least one tRNA.

111. (Currently Amended) The method of claim 109, wherein one of the labels is selected from the group consisting of a fluorescent dye, a fluorescent nucleotide, a quantum dot, and a luminescent substance~~, and the emitted radiation signal comprises a FRET signal, a quenching signal or a fluorescent signal~~.

112. (Previously Presented) The method of claim 109, wherein the first and second labels together comprise a donor-quencher pair or a fluorescent donor-acceptor pair.

113. (Previously Presented) The method of claim 109, which further comprises irradiating the system with electromagnetic radiation prior to the step of detecting the emitted radiation signals, and a plurality of proteins are identified.

114. (Previously Presented) The method of claim 109, wherein the analyzing of the emitted radiation signals comprises:

clustering the signals into a list of protein signal sequences;

transforming the signal sequences into at least one data stream; and

recording the data stream in the signal database.

115. (Previously Presented) The method of claim 114, wherein said signal sequences are composed of one or more values selected from the group consisting of time, spatial coordinates, signal type and signal intensity.

116. (Previously Presented) The method of claim 109, which is conducted in a cell or in an in-vitro translation system, and the ribosomal fragment is selected from the group consisting of ribosomal RNA and a ribosomal protein, and the detecting is performed in real time.

117. (Previously Presented) The method of claim 109, which is conducted in a cell from an organism higher than prokaryotic bacteria.

118. (Previously Presented) The method of claim 117, wherein the synthesis of the one or more proteins is indicative of a pathological condition in the organism.

119. (Previously Presented) The method of claim 117, further comprising subjecting the cell to an external stimulus, and monitoring the response of the protein synthesis apparatus of the cell to the external stimulus.

120. (Previously Presented) The method of claim 109, wherein the detecting is carried out over a period of time.

121. (Previously Presented) The method of claim 120, wherein the period of time corresponds to the synthesis cycle time of a single amino acid.

122. (New) The method of claim 109, wherein the computing of the synthesis signal comprises:

recording beginning and end points for each FRET signal time period;

computing probabilities of labeled sequences based on the type of signals recorded and the time differences of the recorded beginning and end points; and

generating labeled sequences from the computed probabilities based on the interrogation of the database.

123. (New) The method of claim 122, wherein the computing of the probabilities of labeled sequences is based on time differences of the recorded beginning and end points.